



Article

Transcriptomic evidence of molecular mechanisms underlying the response of *Lactobacillus plantarum* WCFS1 to hydroxytyrosol

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**Table 1.** Oligonucleotides used for qRT-PCR in this study designed with Primer Express 3.0 software.

Locus Tag ^a	Locus	Description	Primer sequence (5' → 3')	Expression ratios ^d	
				Microarray ^e	RT-qPCR ^f
lp_2108	<i>cps4A</i>	polysaccharide biosynthesis protein, chain length regulator	F ^b : TTGGGCGGGACGATTG R ^c : GCTTGATATTCGGGCTGAATG	1.05	0.17
lp_0255	<i>metC1</i>	cystathionine beta-lyase / cystathionine gamma-lyase	F: TTGGCCCCGCAAGAAA R: ATGCGCAATGCCAGAGTCT	1.03	0.55
lp_0843	<i>ppx3</i>	exopolyphosphatase	F: GCCGTTTGCCACCCTCTT R: GTTCCTCCACGCCAGCTTT	1.1	0.32
lp_0927	—	membrane protein	F: CCAACAGGCGGCAACCT R: TTCGACCGTCAATCCCAATT	1.18	0.08
lp_0291	—	glycolate dehydrogenase, subunit GlcD, FAD-binding	F: CCGGACCCTGGTTCTAAGC R: GGCGTTTGTCGCCACATTAC	1.04	0.78
lp_3184	—	branched-chain amino acid transport protein	F: TGGCTTTCATACCACGCTTTT R: TTGGGATCTTCCGCTTCGT	-1.76	-2.54
lp_2525	—	ABC transporter ATP-binding protein	F: GCAGCGCAACGTTTCGAA R: ATGCCGGCTGGAATATCG	-1.71	-3.23
lp_3254	<i>lrgA</i>	murein hydrolase export protein	F: AGGTGGCGGGTGTTAGCA R: TCCCTGATGGAATGAAAATCAAG	-1.94	-3.92
lp_0349	<i>amtB</i>	ammonium transport protein	F: GGCATGGTCGGCAGTATCAT R: TTGTGCGATTAACGGCTTTG	-1.77	-2.9
lp_2740	—	ABC transporter permease	F: CAACCTAACCGGCCACAAC R: GACACCGACGACAATTTTCA	-1.94	-4.47
Housekeeping and others internal control genes					
lp_2057	<i>ldhD</i>	D-lactate dehydrogenase	F: AACCGCGACAATGTTTTGATT R: TTGTGAACGGCAGTTTCAGTGT	-1.47	-2.96
lp_0789	<i>gapB</i>	glyceraldehyde 3-phosphate dehydrogenase	F: CTGGTGCTGCTAAGGCTCTTG R: TGTGCATGGCCTTGTAATTTACC	-0.25	-1.35
lp_1963	<i>dnaG</i>	DNA primase DnaG	F: TCCGGAAGCAGTCGTCAAG R: TCGCCGGCAAGTCAATGT	-0.13	-1.19
lp_0007	<i>gyrA</i>	DNA gyrase, A subunit	F: CCCGACAGCAACGTCTTCA R: GGCAGCTGGCGTTTGT	-0.05	-1.09



lp_1962	<i>rpoD</i>	RNA polymerase sigma factor RpoD	F: CGGATCCGCCAAATCG R: CGTGATGGGTGGCGTAACTT	0.03	0.98
lp_0006	<i>gyrB</i>	DNA gyrase, B subunit	F: CCCGGGTCGCTGCTAAG R: TTTCCAAGCCACTCTTTTTTCG	0.27	-0.67
lp_2301	<i>recA</i>	recombinase A	F: CGGCGGGCAGAACAGAT R: TTTCCAAGCCACTCTTTTTTCG	-1.1	-2.47
lp_1021	<i>rpoB</i>	DNA-directed RNA polymerase subunit beta	F: GGGTGTGCCTTCTCGTATGAA R: CAGCCATCCCCAAATGCA	0.02	-1.0
lp_rRNA01	16srRNA	16S ribosomal rRNA	F: GGGTAATCGGCCACATTGG R: CTGCTGCCTCCCGTAGGA	0.26	-0.68

^a Designated gene number for the annotated *L. plantarum* WCFS1 genome. ^b Forward. ^c Reverse. ^d Genes ratios >1.5 fold changes (either increase or decrease) were statistically significant ($p < 0.05$). ^e $\log_2\text{ratio}(M)$, where $\text{ratio}(M)$ = fold change. ^f $\log_2$ ratios of average fold change.

Table 2. *Lactobacillus plantarum* WCFS1 genes with differential expression in presence of 10 mM hydroxytyrosol.

Gene ID	Locus	Description	COGs	Fold Change ^{a,b}	Subcellular Localization Prediction ^c	Pathway Prediction ^c
lp_0011	<i>rpsR</i>	30S ribosomal protein S18	J: Translation, ribosomal structure and biogenesis	-2,15	Intracellular	
lp_0030	–	pyridoxamine 5'-phosphate oxidase family protein, FMN-binding	–	-1,63	Intracellular	
lp_0032	–	hypothetical protein	–	-1,9	Intracellular	
lp_0039	–	regulator of two-component system, YycI family	S: Function unknown	-1,93	N-terminally anchored (No CS)	Sec-(SPI)
lp_0047	<i>aldH</i>	coniferyl aldehyde dehydrogenase	C: Energy production and conversion	1,65	Intracellular	
lp_0052	–	6-pyruvoyl-tetrahydropterin synthase	H: Coenzyme transport and metabolism	-1,78	Intracellular	
lp_0069	<i>ptp1</i>	protein-tyrosine phosphatase	T: Signal transduction mechanisms	-1,7	Intracellular	
lp_0099	–	hypothetical protein	–	-1,87	Intracellular	
lp_0111		medium chain dehydrogenases/reductase (MDR)/zinc-dependent alcohol dehydrogenase	C: Energy production and conversion	-1,76	Intracellular	
lp_0119	–	NTP pyrophosphohydrolase	F: Nucleotide transport and metabolism	1,84	Intracellular	
lp_0120	–	amino acid/polyamine transport protein, APC	E: Amino acid transport and metabolism	-2,47	Multi-transmembrane	Sec-(SPI)
lp_0124	<i>pacL1</i>	cation transporting P-type ATPase	P: Inorganic ion transport and metabolism	-2,02	Multi-transmembrane	Sec-(SPI)
lp_0127	–	NADPH-dependent FMN reductase	R: General function prediction only	1,69	Intracellular	
lp_0151	–	no items found	–	-2,21	Intracellular	
lp_0159	–	short-chain dehydrogenase/oxidoreductase	I: Lipid transport and metabolism	1,70	Intracellular	
lp_0202	–	GNAT family acetyltransferase	–	-1,84	Intracellular	
lp_0215	–	ABC transporter ATP-binding protein	R: General function prediction only	-2,03	Intracellular	

lp_0230	<i>pts2CB</i>	PTS system, mannitol-specific EIICB component	G: Carbohydrate transport and metabolism	1,91	Multi-transmembrane	Sec-(SPI)
lp_0244	–	NADPH-dependent FMN reductase	R: General function prediction only	-2,23	Intracellular	
lp_0255	<i>metC1</i>	cystathionine beta-lyase / cystathionine gamma-lyase	E: Amino acid transport and metabolism	2,20	Intracellular	
lp_0256	<i>cysK</i>	cystathionine beta-synthase	E: Amino acid transport and metabolism	1,91	Intracellular	
lp_0257	<i>pepM</i>	methionyl aminopeptidase	J: Translation, ribosomal structure and biogenesis	-1,67	Intracellular	
lp_0261	–	membrane protein	–	-1,92	Multi-transmembrane	Sec-(SPI)
lp_0265	<i>pts5ABC</i>	PTS system trehalose-specific transporter subunit IIBC	G: Carbohydrate transport and metabolism	-2,77	Multi-transmembrane	Sec-(SPI)
lp_0272	–	aromatic acid carboxylase, subunit D	–	-1,56	Intracellular	
lp_0274	–	TetR family transcriptional regulator	K: Transcription	1,55	Intracellular	
lp_0286	<i>pts6C</i>	PTS system, cellobiose-specific EIIC component	G: Carbohydrate transport and metabolism	-1,83	Multi-transmembrane	Sec-(SPI)
lp_0291	–	glycolate dehydrogenase, subunit GlcD,FAD-binding	C: Energy production and conversion	2,05	Intracellular	
lp_0292	–	hypothetical protein	–	2,11	Intracellular	
lp_0293	–	GTP pyrophosphokinase	S: Function unknown	1,5	Intracellular	
lp_0295	–	transport protein, MMPL family	R: General function prediction only	1,71	Multi-transmembrane	Sec-(SPI)
lp_0302	–	extracellular transglycosylase	–	-1,67	N-terminally anchored (No CS)	Sec-(SPI)
lp_0312	–	MarR family transcriptional regulator	K: Transcription	1,75	Intracellular	
lp_0325	–	acetoin transport repressor, GntR family	K: Transcription	-1,68	Intracellular	
lp_0327	–	acetoin ABC transporter, permease protein	–	-2,64	Multi-transmembrane	Sec-(SPI)
lp_0349	<i>amtB</i>	ammonium transport protein	P: Inorganic ion transport and metabolism	-3,40	Multi-transmembrane	Sec-(SPI)
lp_0402	–	hypothetical protein	–	-1,93	Intracellular	
lp_0444	–	hypothetical protein	–	1,85	Intracellular	
lp_0455	–	drug resistance transpor protein, major facilitator superfamily (MFS), Bcr/CflA subfamily	G: Carbohydrate transport and metabolism	-1,71	Multi-transmembrane	Sec-(SPI)

lp_0464	_	zinc/iron ABC transporter, permease protein	P: Inorganic ion transport and metabolism	-2,02	Multi-transmembrane	Sec-(SPI)
lp_0467	<i>glmU</i>	UDP-N-acetylglucosamine pyrophosphorylase	M: Cell wall/membrane/envelope biogenesis	-1,72	Intracellular	
lp_0477	_	lipoate-protein ligase A	H: Coenzyme transport and metabolism	-1,57	Intracellular	
lp_0484	<i>rimK</i>	ATP-dependent carboxylate-amine/thiol ligase	H: Coenzyme transport and metabolism	1,49	Intracellular	
lp_0509	_	hypothetical protein	_	-1,99	Intracellular	
lp_0514	<i>srtA</i>	sortase A	M: Cell wall/membrane/envelope biogenesis	1,70	N-terminally anchored (No CS)	Sec-(SPI)
lp_0535	_	hypothetical protein	T: Signal transduction mechanisms	-2,07	Intracellular	
lp_0543	_	RNA binding protein, contains ribosomal protein S1 domain	J: Translation, ribosomal structure and biogenesis	-2,57	Intracellular	
lp_0551	<i>dtpT</i>	di-/tripeptide transport protein	E: Amino acid transport and metabolism	-2,58	Multi-transmembrane	Sec-(SPI)
lp_0555	_	hypothetical protein	_	2	Intracellular	
lp_0584	_	transport protein, major facilitator superfamily (MFS)	_	-1,49	Multi-transmembrane	Sec-(SPI)
lp_0594	<i>mleP1</i>	malate transport protein	R: General function prediction only	-1,73	Multi-transmembrane	Sec-(SPI)
lp_0595	_	permease, drug/metabolite transporter (DMT) superfamily	S: Function unknown	-1,72	Multi-transmembrane	Sec-(SPI)
lp_0694	<i>nrdH</i>	glutaredoxin-like protein nrdH	O: Posttranslational modification, protein turnover, chaperones	-1,86	Intracellular	
lp_0701	_	hypothetical protein	_	-2,37	Intracellular	
lp_0726	_	membrane-bound protease, CAAX family	R: General function prediction only	-1,91	Multi-transmembrane	Sec-(SPI)
lp_0727	<i>groES</i>	GroES co-chaperonin Cpn10	O: Posttranslational modification, protein turnover, chaperones	2	Intracellular	

lp_0728	<i>groEL</i>	GroEL chaperonin Cpn60	O: Posttranslational modification, protein turnover, chaperones	1,75	Intracellular	
lp_0742	_	membrane protein	O: Posttranslational modification, protein turnover, chaperones	1,65	Multi-transmembrane	Sec-(SPI)
lp_0753	_	membrane protein	S: Function unknown	-1,61	Multi-transmembrane	Sec-(SPI)
lp_0755	<i>lgt</i>	Prolipoprotein diacylglyceryl transferase	M: Cell wall/membrane/envelope biogenesis	1,71	Multi-transmembrane	Sec-(SPI)
lp_0758	_	diguanylate cyclase/phosphodiesterase, EAL domain	T: Signal transduction mechanisms	1,71	Intracellular	
lp_0787	<i>rpoN</i>	DNA-directed RNA polymerase, sigma factor 54	K: Transcription	-1,61	Intracellular	
lp_0792	<i>eno</i>	Enolase 1 (phosphopyruvate hydratase) 2-phospho-D-glycerate hydro-lyase 1 2-phosphoglycerate dehydratase 1	G: Carbohydrate transport and metabolism	-1,83	Intracellular	
lp_0799	<i>smpB</i>	SsrA-binding protein Small protein B SSRA RNA binding protein	O: Posttranslational modification, protein turnover, chaperones	-1,96	Intracellular	
lp_0802	<i>glnPH1</i>	polar amino acid ABC transporter, substrate binding and permease protein	E: Amino acid transport and metabolism	-2,16	Multi-transmembrane	Sec-(SPI)
lp_0803	<i>glnQ1</i>	glutamine ABC transporter ATP-binding protein	E: Amino acid transport and metabolism	-2,72	Intracellular	
lp_0811	_	DNA-directed DNA polymerase III subunit epsilon	L: Replication, recombination and repair	-1,58	Intracellular	
lp_0816	_	MarR family transcriptional regulator	K: Transcription	-1,57	Intracellular	
lp_0817	_	membrane protein	S: Function unknown	-2,07	Multi-transmembrane	Sec-(SPI)
lp_0820	<i>glmM</i>	Phosphoglucosamine mutase	G: Carbohydrate transport and metabolism	-1,98	Intracellular	
lp_0828	_	hypothetical protein	_	1,81	Intracellular	
lp_0842	<i>ppk</i>	Polyphosphate kinase ATP-polyphosphate phosphotransferase Polyphosphoric acid kinase	P: Inorganic ion transport and metabolism	1,52	Intracellular	
lp_0843	<i>ppx3</i>	exopolyphosphatase	F: Nucleotide transport and metabolism	2,13	Intracellular	
lp_0848	_	purine transport protein	R: General function prediction only	-1,85	Intracellular	

lp_0856	_	acyltransferase	I: Lipid transport and metabolism	-2,09	Multi-transmembrane	Sec-(SPI)
lp_0858	_	redox protein, regulator of disulfide bond formation	O: Posttranslational modification, protein turnover, chaperones	1,66	Intracellular	
lp_0865	_	hypothetical protein	_	-2,35	Intracellular	
lp_0882	<i>glnM</i>	glutamine ABC transporter, permease protein	E: Amino acid transport and metabolism	1,59	Multi-transmembrane	Sec-(SPI)
lp_0899	_	membrane protein	_	-1,9	Multi-transmembrane	Sec-(SPI)
lp_0927	_	membrane protein	_	2,26	Multi-transmembrane	Sec-(SPI)
lp_0928	_	hypothetical protein	_	1,99	N-terminally anchored (No CS)	Sec-(SPI)
lp_0929	<i>asp1</i>	alkaline shock protein	S: Function unknown	1,84	Intracellular	
lp_0930	<i>asp2</i>	alkaline shock protein	S: Function unknown	1,98	Intracellular	
lp_0940	<i>hsdS1</i>	type I restriction-modification system, specificity subunit	V: Defense mechanisms	-2,03	Intracellular	
lp_0956	<i>asnC</i>	Asparagine--tRNA ligase 1 Asparaginyl-tRNA synthetase 1AsnRS 1	J: Translation, ribosomal structure and biogenesis	-1,85	Intracellular	
lp_0963	<i>rluE</i>	ribosomal large subunit pseudouridine synthase	J: Translation, ribosomal structure and biogenesis	-1,54	Intracellular	
lp_0994	_	no items found	_	-4,11	Intracellular	
lp_1005	<i>als</i>	acetolactate synthase	E: Amino acid transport and metabolism	1,63	Intracellular	
lp_1011	<i>dgk1</i>	deoxyadenosine kinase / deoxyguanosine kinase	F: Nucleotide transport and metabolism	1,82	Intracellular	
lp_1027	<i>fusA2</i>	Elongation factor G EF-G	J: Translation, ribosomal structure and biogenesis	-2,21	Intracellular	
lp_1054	<i>rpmD</i>	50S ribosomal protein L30	J: Translation, ribosomal structure and biogenesis	1,63	Intracellular	
lp_1063	<i>rplQ</i>	50S ribosomal protein L17	J: Translation, ribosomal structure and biogenesis	-2,35		
lp_1068	_	extracellular protein	S: Function unknown	-1,5	N-terminally anchored (No CS)	Sec-(SPI)
lp_1070	_	lipoprotein precursor, FMN-binding protein	S: Function unknown	-1,91	Lipid anchored	Sec-(SPII)

lp_1078	<i>rpsI</i>	30S ribosomal protein S9	J: Translation, ribosomal structure and biogenesis	-2,39	Intracellular	
lp_1096	<i>mtsB</i>	manganese ABC transporter, permease protein	P: Inorganic ion transport and metabolism	-1,87	Multi-transmembrane	Sec-(SPI)
lp_1097	<i>mtsA</i>	manganese/zinc ABC transporter, substrate binding protein	P: Inorganic ion transport and metabolism	-1,55	N-terminally anchored (No CS)	Sec-(SPI)
lp_1101	<i>ldh</i>	L-lactate dehydrogenase 2 L-LDH 2	C: Energy production and conversion	1,58	Intracellular	
lp_1116	<i>mleR1</i>	malolactic regulator, LysR family	K: Transcription	1,81	Intracellular	
lp_1120	–	amino acid transport protein	E: Amino acid transport and metabolism	-2,23	Multi-transmembrane	Sec-(SPI)
lp_1136	–	oxidoreductase, NAD(P)-dependent	R: General function prediction only	1,83	Intracellular	
lp_1150	–	diacylglycerol kinase family protein	R: General function prediction only	-1,64	Intracellular	
lp_1174	–	ribonuclease BN family protein	S: Function unknown	-1,85	Multi-transmembrane	Sec-(SPI)
lp_1190	<i>rfbD</i>	dTDP-4-dehydrorhamnose reductase	M: Cell wall/membrane/envelope biogenesis	-1,98	Intracellular	
lp_1215	<i>cps3A</i>	glycosyltransferase, family 2 (GT2)	R: General function prediction only	1,56	Intracellular	
lp_1229	–	mannose-specific adhesin, LPXTG-motif cell wall anchor	–	-1,83	LPxTG Cell-wall anchored	Sec-(SPI)
lp_1230	–	MarR family transcriptional regulator	K: Transcription	-1,95	Intracellular	
lp_1244	–	hypothetical protein	–	-1,88	Intracellular	
lp_1245	<i>hicD2</i>	L-2-hydroxyisocaproate dehydrogenase	C: Energy production and conversion	-1,75	Intracellular	
lp_1248	<i>tagD2</i>	glycerol-3-phosphate cytidylyltransferase	M: Cell wall/membrane/envelope biogenesis	-1,89	Intracellular	
lp_1259	–	anion exporter, TauE/SafE family	R: General function prediction only	1,73	Multi-transmembrane	Sec-(SPI)
lp_1280	<i>araT1</i>	aromatic amino acid specific aminotransferase	E: Amino acid transport and metabolism	-1,73	Intracellular	
lp_1292	–	GNAT family acetyltransferase	J: Translation, ribosomal structure and biogenesis	-2,5	Intracellular	

lp_1297	_	S-methylmethionine transport protein	E: Amino acid transport and metabolism	-1,51	Multi-transmembrane	Sec-(SPI)
lp_1300	_	membrane protein	_	-1,89	Multi-transmembrane	Sec-(SPI)
lp_1333	_	hypothetical protein	_	-1,58	Intracellular	
lp_1334	_	ABC transporter permease	_	-1,72	Multi-transmembrane	Sec-(SPI)
lp_1360	_	MarR family transcriptional regulator	K: Transcription	-1,79	Intracellular	
lp_1363	_	hypothetical protein	_	-1,53	Intracellular	
lp_1372	<i>gtcA1</i>	teichoic acid glycosylation protein	S: Function unknown	-1,71	Multi-transmembrane	Sec-(SPI)
lp_1388	_	hypothetical protein	_	-1,79	Intracellular	
lp_1394	_	hypothetical protein, N-terminus (pseudogene)	_	1,69	Intracellular	
lp_1406	<i>dltC2</i>	D-alanine--poly(phosphoribitol) ligase subunit 2-2 Full=D-alanyl carrier protein 2 DCP 2	I: Lipid transport and metabolism	-2,11	Intracellular	
lp_1427	_	nucleoside 2-deoxyribosyltransferase	F: Nucleotide transport and metabolism	-1,57	Intracellular	
lp_1436		riboflavin synthase, alpha chain		1,64		
lp_1437	<i>ribA</i>	3,4-dihydroxy-2-butanone 4-phosphate synthase /GTP cyclohydrolase II	H: Coenzyme transport and metabolism	1,95	Intracellular	
lp_1442	_	Crp/FNR family transcriptional regulator	T: Signal transduction mechanisms	-1,63	Intracellular	
lp_1445	<i>npr1</i>	NADH peroxidase	R: General function prediction only	-1,73	Intracellular	
lp_1468	_	ABC transporter, ATP-binding protein,iron-sulfur cluster assembly ATPase protein SufC	O: Posttranslational modification, protein turnover, chaperones	1,61	Intracellular	
lp_1483	_	Xre family transcriptional regulator	_	-1,67	Intracellular	
lp_1515	<i>infC</i>	Translation initiation factor IF-3	J: Translation, ribosomal structure and biogenesis	1,76	Intracellular	
lp_1517	<i>rplT</i>	50S ribosomal protein L20	J: Translation, ribosomal structure and biogenesis	-1,94	Intracellular	
lp_1544	<i>rrp5</i>	two-component system response regulator	T: Signal transduction mechanisms	-1,82	Intracellular	
lp_1545	<i>hpk5</i>	two-component system histidine protein kinase; sensor protein	T: Signal transduction mechanisms	-1,96	Multi-transmembrane	Sec-(SPI)
lp_1567	_	membrane protein	S: Function unknown	-1,7	Multi-transmembrane	Sec-(SPI)

lp_1573	<i>glk</i>	bifunctional protein: transcription regulator; sugar kinase, ROK family	K: Transcription	-2,18	Intracellular	
lp_1581	<i>glnA</i>	glutamate--ammonia ligase	E: Amino acid transport and metabolism	-2,73	Intracellular	
lp_1594	<i>rpmA</i>	50S ribosomal protein L27	J: Translation, ribosomal structure and biogenesis	-2,59	Intracellular	
lp_1613	<i>rpoZ</i>	DNA-directed RNA polymerase subunit omega	K: Transcription	-1,87	Intracellular	
lp_1622	–	thiamin pyrophosphokinase	H: Coenzyme transport and metabolism	-2,23	Intracellular	
lp_1626	–	phosphatase, dihydroxyacetone kinase family	R: General function prediction only	-2,02	Intracellular	
lp_1637	–	RNA binding protein	R: General function prediction only	-2,19	Intracellular	
lp_1640	<i>rplS</i>	50S ribosomal protein L19	J: Translation, ribosomal structure and biogenesis	-1,69	Intracellular	
lp_1687	–	Putative ribosome biogenesis GTPase RsgA 2 ribosome small subunit-dependent GTPase A	R: General function prediction only	-1,91	Intracellular	
lp_1702	–	membrane protein	S: Function unknown	-2,34	Multi-transmembrane	Sec-(SPI)
lp_1713	<i>lysA</i>	diaminopimelate decarboxylase	E: Amino acid transport and metabolism	-1,78	Intracellular	
lp_1722	–	4-aminobutanoate transport protein	E: Amino acid transport and metabolism	-1,72	Multi-transmembrane	Sec-(SPI)
lp_1732	<i>idi1</i>	isopentenyl diphosphate delta-isomerase	C: Energy production and conversion	-2,07	Intracellular	
lp_1742	–	hypothetical protein	–	-1,7	Intracellular	
lp_1757	–	ArsR family transcriptional regulator	K: Transcription	-1,99	Intracellular	
lp_1767	–	glycosyl hydrolase family protein	–	-1,85	Secretory(released) (with CS)	Sec-(SPI)
lp_1771	–	ABC transporter ATP-binding protein	P: Inorganic ion transport and metabolism	-1,79	Intracellular	
lp_1773	–	membrane protein	–	-2,33	Multi-transmembrane	Sec-(SPI)
lp_1778	<i>esbA</i>	membrane protein	–	1,7	Multi-transmembrane	Sec-(SPI)
lp_1787	<i>cat</i>	chloramphenicol O-acetyltransferase	V: Defense mechanisms	-1,87	Intracellular	
lp_1793	–	fibrinogen-binding family protein	K: Transcription	-1,64	Intracellular	

lp_1818	<i>tagB1</i>	ribitolphosphotransferase	M: Cell wall/membrane/envelope biogenesis	1,68	Intracellular	
lp_1836	<i>msrA3</i>	protein-methionine-S-oxide reductase	O: Posttranslational modification, protein turnover, chaperones	1,94	Intracellular	
lp_1869	<i>dfrA</i>	dihydrofolate reductase	H: Coenzyme transport and metabolism	1,71	Intracellular	
lp_1879	<i>hbsU</i>	DNA-binding protein	L: Replication, recombination and repair	-2,12	Intracellular	
lp_1881	<i>engA</i>	ribosome-associated GTPase	R: General function prediction only	-1,72	Intracellular	
lp_1887	—	riboflavin transporter	S: Function unknown	-2,24	Multi-transmembrane	Sec-(SPI)
lp_1898	<i>pfkA</i>	6-phosphofructokinase	G: Carbohydrate transport and metabolism	1,72	Intracellular	
lp_1914	—	MarR family transcriptional regulator	K: Transcription	1,53	Intracellular	
lp_1948	—	MarR family transcriptional regulator	K: Transcription	1,81	Intracellular	
lp_1953	—	hypothetical protein	—	-1,71	Intracellular	
lp_1956	—	ABC transporter permease	—	-2,01	Multi-transmembrane	Sec-(SPI)
lp_1972	—	hypothetical protein	S: Function unknown	-2,09	Intracellular	
lp_1982	<i>lytH</i>	N-acetylmuramoyl-L-alanine amidase	M: Cell wall/membrane/envelope biogenesis	-2,14		
lp_1985	—	phosphohydrolase	R: General function prediction only	-1,91	Intracellular	
lp_1988	—	membrane protein	—	-1,82	Multi-transmembrane	Sec-(SPI)
lp_1997	—	integrase, fragment	L: Replication, recombination and repair	-1,54	Intracellular	
lp_2001	—	membrane protein	—	-2,77	Multi-transmembrane	Sec-(SPI)
lp_2039	<i>rbfA</i>	ribosome-binding factor A	J: Translation, ribosomal structure and biogenesis	-2,19	Intracellular	
lp_2056	—	HAD-superfamily hydrolase	R: General function prediction only	-1,74	Intracellular	
lp_2057	<i>ldhD</i>	D-lactate dehydrogenase D-LDH	C: Energy production and conversion	-2,77	Intracellular	

lp_2066	–	hypothetical protein	–	-2,03	Multi-transmembrane	Sec-(SPI)
lp_2086	<i>apt</i>	Adenine phosphoribosyltransferase APRT	F: Nucleotide transport and metabolism	-1,71	Intracellular	
lp_2105	<i>galE3</i>	UDP N-acetyl glucosamine 4-epimerase, NAD dependent	M: Cell wall/membrane/envelope biogenesis	1,67	Intracellular	
lp_2108	<i>cps4A</i>	polysaccharide biosynthesis protein, chain length regulator	M: Cell wall/membrane/envelope biogenesis	2,07	Multi-transmembrane	Sec-(SPI)
lp_2110	<i>glnQ3</i>	glutamine ABC transporter ATP-binding protein	E: Amino acid transport and metabolism	-1,7	Intracellular	
lp_2114	–	NTP pyrophosphohydrolase	R: General function prediction only	-2,72	Intracellular	
lp_2122	–	metallo-beta-lactamase superfamily protein	R: General function prediction only	-2,17	Intracellular	
lp_2125	<i>rpsO</i>	30S ribosomal protein S15	J: Translation, ribosomal structure and biogenesis	-2,64	Intracellular	
lp_2126	<i>rpsT</i>	30S ribosomal protein S20	J: Translation, ribosomal structure and biogenesis	-2,48	Intracellular	
lp_2133	<i>coaD</i>	pantetheine-phosphate adenylyltransferase	H: Coenzyme transport and metabolism	1,84	Intracellular	
lp_2162	–	extracellular protein, NlpC/P60 family, gamma-D-glutamate-meso-diaminopimelate murepeptidase	M: Cell wall/membrane/envelope biogenesis	-2,04	N-terminally anchored (No CS)	Sec-(SPI)
lp_2199	<i>mraY</i>	Phospho-N-acetylmuramoyl-pentapeptide-transferase UDP-MurNAc-pentapeptide phosphotransferase	M: Cell wall/membrane/envelope biogenesis	-2,30	Multi-transmembrane	Sec-(SPI)
lp_2201	<i>ftsL</i>	cell division protein FtsL	D: Cell cycle control, cell division, chromosome partitioning	-1,53	N-terminally anchored (No CS)	Sec-(SPI)
lp_2215	<i>rrmA</i>	rRNA large subunit methyltransferase A	H: Coenzyme transport and metabolism	-1,67	Intracellular	
lp_2229	–	beta-lactamase superfamily metal-dependent hydrolase	R: General function prediction only	-2,02	Intracellular	
lp_2230	–	hypothetical protein	–	-1,73	Intracellular	

lp_2240	_	amino acid transport protein	E: Amino acid transport and metabolism	-2,38	Multi-transmembrane	Sec-(SPI)
lp_2270	<i>trxA2</i>	thioredoxin	O: Posttranslational modification, protein turnover, chaperones	-1,81	Intracellular	
lp_2273	_	hypothetical protein UPF0473	S: Function unknown	-1,71	Intracellular	
lp_2277	<i>alaS</i>	Alanine--tRNA ligase Alanyl-tRNA synthetase AlaRS	J: Translation, ribosomal structure and biogenesis	-1,75	Intracellular	
lp_2278	<i>rhe3</i>	ATP-dependent RNA helicase	L: Replication, recombination and repair	-1,58	Intracellular	
lp_2281	_	preprotein translocase subunit YajC	U: Intracellular trafficking, secretion, and vesicular transport	-1,79	N-terminally anchored (No CS)	Sec-(SPI)
lp_2308	<i>thrA2</i>	aspartate kinase	E: Amino acid transport and metabolism	-1,8	Intracellular	
lp_2317	<i>mreD</i>	cell shape determining protein MreD	M: Cell wall/membrane/envelope biogenesis	-1,61	Multi-transmembrane	Sec-(SPI)
lp_2334	_	membrane protein	_	-2,12	Multi-transmembrane	Sec-(SPI)
lp_2341	<i>bla2</i>	beta-lactamase, class A	V: Defense mechanisms	-1,61	N-terminally anchored (No CS)	Sec-(SPI)
lp_2342	_	Xre family transcriptional regulator	_	-2,09	Intracellular	
lp_2346	_	alcohol dehydrogenase	C: Energy production and conversion	1,49	Intracellular	
lp_2347	_	hypothetical protein	_	1,55	Intracellular	
lp_2365	<i>atpG</i>	ATP synthase gamma chain ATP synthase F1 sector gamma subunit F-ATPase gamma subunit	C: Energy production and conversion	1,78	Intracellular	
lp_2367	<i>atpH</i>	ATP synthase subunit delta ATP synthase F(1) sector subunit delta F-type ATPase subunit delta F-ATPase subunit delta	C: Energy production and conversion	1,60	Intracellular	
lp_2368	<i>atpF</i>	ATP synthase subunit b ATP synthase F(0) sector subunit b ATPase subunit I F-type ATPase subunit b F-ATPase subunit b	C: Energy production and conversion	1,55	N-terminally anchored (No CS)	Sec-(SPI)
lp_2378	<i>prfA</i>	peptide chain release factor 1	J: Translation, ribosomal structure and biogenesis	-1,7	Intracellular	

lp_2390	<i>bcaT</i>	branched-chain amino acid aminotransferase	E: Amino acid transport and metabolism	-1,96	Intracellular	
lp_2443	_	prophage P2a protein 14	S: Function unknown	-1,53	Intracellular	
lp_2454	_	prophage P2a protein 3; DNA adenine methylase	L: Replication, recombination and repair	-1,97	Intracellular	
lp_2502	<i>pgi</i>	glucose-6-phosphate isomerase	G: Carbohydrate transport and metabolism	-2,05	Intracellular	
lp_2516	_	hypothetical protein	_	-2,58	Intracellular	
lp_2525	_	ABC transporter ATP-binding protein	R: General function prediction only	-3,27	Intracellular	
lp_2531	<i>pts18CBA</i>	PTS system, N-acetylglucosamine and glucose-specific EIICBA component	G: Carbohydrate transport and metabolism	-2,29	Multi-transmembrane	Sec-(SPI)
lp_2544	<i>npr2</i>	NADH peroxidase	R: General function prediction only	1,86	Intracellular	
lp_2580	_	sulfatase, alkaline phosphatase superfamily, membrane-bound	M: Cell wall/membrane/envelope biogenesis	-1,72	Multi-transmembrane	Sec-(SPI)
lp_2596	<i>pflA1</i>	formate acetyltransferase activating enzyme	O: Posttranslational modification, protein turnover, chaperones	1,81	Intracellular	
lp_2613	_	ABC transporter permease	_	-3,42	Multi-transmembrane	Sec-(SPI)
lp_2614	_	ABC transporter ATP-binding protein	V: Defense mechanisms	-2,06	Intracellular	
lp_2615	_	GntR family transcriptional regulator	K: Transcription	-2,04	Intracellular	
lp_2631	_	lipase/esterase	E: Amino acid transport and metabolism	-1,84	Intracellular	
lp_2642	_	membrane protein	_	1,55	Multi-transmembrane	Sec-(SPI)
lp_2647	<i>pts19A</i>	PTS system, N-acetylglucosamine/galactosamine-specific EIIA component	G: Carbohydrate transport and metabolism	-2,04	Intracellular	
lp_2659	<i>xpk1</i>	xylulose-5-P phosphoketolase / fructose-6-P phosphoketolase	G: Carbohydrate transport and metabolism	1,69	Intracellular	
lp_2664	_	metal-dependent phosphohydrolase, HD family	R: General function prediction only	1,68	Intracellular	
lp_2710	<i>pucK</i>	xanthine permease	F: Nucleotide transport and metabolism	-2,48	Multi-transmembrane	Sec-(SPI)

lp_2716	<i>ica3</i>	family 2 glycosyltransferase	M: Cell wall/membrane/envelope biogenesis	-1,58	Multi-transmembrane	Sec-(SPI)
lp_2727	<i>purC</i>	Phosphoribosylaminoimidazole-succinocarboxamide synthase SAICAR synthetase	F: Nucleotide transport and metabolism	1,62	Intracellular	
lp_2735	<i>ptp3</i>	protein-tyrosine phosphatase	T: Signal transduction mechanisms	1,71	Intracellular	
lp_2738	–	L-asparaginase	E: Amino acid transport and metabolism	1,535	Intracellular	
lp_2739	–	ABC transporter ATP-binding protein	V: Defense mechanisms	-4,73	Intracellular	
lp_2740	–	ABC transporter permease	Q: Secondary metabolites biosynthesis, transport and catabolism	-3,81	Multi-transmembrane	Sec-(SPI)
lp_2741	–	membrane protein	–	-1,56	Multi-transmembrane	Sec-(SPI)
lp_2742	–	GntR family transcriptional regulator	K: Transcription	-1,84	Intracellular	
lp_2743	–	ABC transporter ATP-binding protein	V: Defense mechanisms	-1,54	Intracellular	
lp_2744	–	ABC transporter permease	–	-3,03	Multi-transmembrane	Sec-(SPI)
lp_2765	–	hypothetical protein	–	1,51	N-terminally anchored (No CS)	Sec-(SPI)
lp_2776	<i>dsdA</i>	Probable D-serine dehydratase D-serine deaminase DSD	E: Amino acid transport and metabolism	-2,57	Intracellular	
lp_2783	–	family 2 glycosyltransferase	M: Cell wall/membrane/envelope biogenesis	-2,04	Intracellular	
lp_2804	–	LysR family transcriptional regulator	K: Transcription	1,77	Intracellular	
lp_2812	–	extracellular protein, membrane-anchored	S: Function unknown	-2,13	N-terminally anchored (No CS)	Sec-(SPI)
lp_2818	–	proton/sodium-glutamate/aspartate symport protein	C: Energy production and conversion	-1,75	Multi-transmembrane	Sec-(SPI)
lp_2823	–	ABC transporter ATP-binding protein	V: Defense mechanisms	-1,78	Intracellular	
lp_2827	<i>napA3</i>	Na(+)/H(+) antiporter	P: Inorganic ion transport and metabolism	-3,51	Multi-transmembrane	Sec-(SPI)
lp_2829	<i>mleP3</i>	malate transport protein	R: General function prediction only	-1,85	Multi-transmembrane	Sec-(SPI)

lp_2830	<i>aspA</i>	aspartate ammonia-lyase	E: Amino acid transport and metabolism	-1,68	Intracellular	
lp_2840	–	ribosomal protein serine-acetylating enzyme	J: Translation, ribosomal structure and biogenesis	-1,5	Intracellular	
lp_2844	<i>tagE6</i>	poly(glycerol-phosphate) alpha-glucosyltransferase	M: Cell wall/membrane/envelope biogenesis	1,6	Intracellular	
lp_2863	<i>sip2</i>	signal peptidase I	U: Intracellular trafficking, secretion, and vesicular transport	-1,56	N-terminally anchored (No CS)	Sec-(SPI)
lp_2888	<i>patB</i>	cystathionine beta-lyase	E: Amino acid transport and metabolism	1,6	Intracellular	
lp_2907	–	GNAT family acetyltransferase	J: Translation, ribosomal structure and biogenesis	1,56	Intracellular	
lp_2912	–	ABC transporter ATP-binding protein	R: General function prediction only	-2,22	Intracellular	
lp_2918	<i>ropB</i>	TetR family transcriptional regulator	K: Transcription	-1,62	Intracellular	
lp_2932	<i>nrdD</i>	anaerobic ribonucleoside-triphosphate reductase	F: Nucleotide transport and metabolism	1,742	Intracellular	
lp_2949	–	membrane protein	–	-1,82	Multi-transmembrane	Sec-(SPI)
lp_2953	–	esterase	R: General function prediction only	1,68	Intracellular	
lp_2960		lipase/esterase, subfamily of SGNH-hydrolases		1,68		
lp_2992	<i>mntH2</i>	manganese transport protein	P: Inorganic ion transport and metabolism	-2,08	Multi-transmembrane	Sec-(SPI)
lp_2993	–	nucleotide-binding protein, universal stress protein UspA family	T: Signal transduction mechanisms	-2,53	Intracellular	
lp_3015	–	extracellular transglycosylase, with LysM peptidoglycan binding domain	M: Cell wall/membrane/envelope biogenesis	-1,66	Secretory(released) (with CS)	Sec-(SPI)
lp_3019	–	extracellular protein, membrane-anchored	–	-1,54	N-terminally anchored (No CS)	Sec-(SPI)
lp_3040	–	multidrug ABC transporter, ATP-binding and permease protein	V: Defense mechanisms	1,88	Multi-transmembrane	Sec-(SPI)
lp_3045	–	short-chain dehydrogenase/oxidoreductase, classical SDR family, subgroup 1	I: Lipid transport and metabolism	-1,58	Intracellular	

lp_3059	–	adherence-associated mucus-binding protein,LPXTG-motif cell wall anchor	–	1,76	LPxTG Cell-wall anchored	Sec-(SPI)
lp_3060	–	AraC family transcriptional regulator	K: Transcription	1,97	Intracellular	
lp_3085	<i>asnB2</i>	asparagine synthase	E: Amino acid transport and metabolism	-2,82	Intracellular	
lp_3087	<i>rrp10</i>	two-component system response regulator	K: Transcription	-1,61	Intracellular	
lp_3096	–	short-chain dehydrogenase	R: General function prediction only	-1,54	N-terminally anchored (No CS)	Sec-(SPI)
lp_3169	–	hypothetical protein	–	-2,31	Intracellular	
lp_3173	–	cell surface protein, membrane-anchored	–	-1,54		
lp_3174	<i>cfa2</i>	cyclopropane-fatty-acyl-phospholipid synthase	M: Cell wall/membrane/envelope biogenesis	-1,58	Intracellular	
lp_3179	–	hypothetical protein	–	-1,67	Intracellular	
lp_3180	–	membrane protein	–	-2,2	Multi-transmembrane	Sec-(SPI)
lp_3183	–	sulfite export protein	–	-1,94	Multi-transmembrane	Sec-(SPI)
lp_3184	–	branched-chain amino acid transport protein	S: Function unknown	-3,38	Multi-transmembrane	Sec-(SPI)
lp_3211	–	cystine ABC transporter ATP-binding protein	E: Amino acid transport and metabolism	-1,95	Intracellular	
lp_3214	–	cystathionine ABC transporter, substrate binding protein	E: Amino acid transport and metabolism	-1,59	Lipid anchored	Sec-(SPII)
lp_3227	–	hypothetical protein	–	-2,02	Intracellular	
lp_3244	–	NADPH-dependent FMN reductase family protein	R: General function prediction only	1,52	Intracellular	
lp_3248	–	bacteriocin immunity protein	–	-1,81	Intracellular	
lp_3254	<i>lrgA</i>	murein hydrolase export protein	R: General function prediction only	-3,81	Multi-transmembrane	Sec-(SPI)
lp_3255	<i>lrgB</i>	murein hydrolase regulator	M: Cell wall/membrane/envelope biogenesis	-2,74	Multi-transmembrane	Sec-(SPI)
lp_3256	–	DegV family protein	S: Function unknown	-1,75	Intracellular	
lp_3267	<i>gshR4</i>	glutathione reductase	C: Energy production and conversion	1,82	Intracellular	
lp_3269	<i>purB</i>	adenylosuccinate lyase	F: Nucleotide transport and metabolism	-1,78	Intracellular	

lp_3286	<i>hly</i>	membrane protein	R: General function prediction only	-1,84	Multi-transmembrane	Sec-(SPI)
lp_3288	_	cation (cobalt-zinc-cadmium) efflux protein	P: Inorganic ion transport and metabolism	-1,59	Multi-transmembrane	Sec-(SPI)
lp_3292	_	hypothetical protein	_	-2,25	Multi-transmembrane	Sec-(SPI)
lp_3312	_	beta-lactamase family protein	V: Defense mechanisms	1,55	Intracellular	
lp_3314	<i>pflA2</i>	formate C-acetyltransferase activating enzyme	O: Posttranslational modification, protein turnover, chaperones	-1,53	Intracellular	
lp_3324	_	glycine betaine/carnitine/choline transport protein	M: Cell wall/membrane/envelope biogenesis	-3,38	Multi-transmembrane	Sec-(SPI)
lp_3334	<i>adeC</i>	Adenine deaminase Adenase Adenine aminase	F: Nucleotide transport and metabolism	-2,48	Intracellular	
lp_3348	_	hypothetical protein	_	-1,79	Intracellular	
lp_3355	_	short-chain dehydrogenase/oxidoreductase, atypical SDR family, subgroup 6	M: Cell wall/membrane/envelope biogenesis	1,75	Intracellular	
lp_3356	_	GNAT family acetyltransferase	R: General function prediction only	1,7	Intracellular	
lp_3378	_	prophage P3 protein 12	_	-1,71	Intracellular	
lp_3382	_	prophage P3 protein 8, DNA primase/helicase	R: General function prediction only	-1,85	Intracellular	
lp_3393	_	cell surface hydrolase, membrane-bound	R: General function prediction only	1,70	N-terminally anchored (No CS)	Sec-(SPI)
lp_3394	_	hypothetical protein	_	1,76	Intracellular	
lp_3397	_	nucleoside 2-deoxyribosyltransferase	F: Nucleotide transport and metabolism	1,59	Intracellular	
lp_3412	_	cell surface protein, CscB family	_	-1,91	N-terminally anchored (No CS)	Sec-(SPI)
lp_3430	_	peroxidase	P: Inorganic ion transport and metabolism	-1,91	Intracellular	
lp_3531	_	LacI family transcriptional regulator	K: Transcription	-1,65	Intracellular	
lp_3552	_	hypothetical protein	J: Translation, ribosomal structure and biogenesis	-1,62	Intracellular	

lp_3558	<i>araR</i>	GntR family transcriptional regulator	K: Transcription	-1,67	Intracellular	
lp_3578	<i>kat</i>	catalase	P: Inorganic ion transport and metabolism	1,70	Intracellular	
lp_3579	<i>nrpR5</i>	RNA polymerase (RNAP)-binding regulatory protein, arsenate reductase (ArsC) family, Spx subfamily	P: Inorganic ion transport and metabolism	-2,04	Intracellular	
lp_3587	<i>pox4</i>	pyruvate oxidase	E: Amino acid transport and metabolism	1,62	Intracellular	
lp_3665	<i>pdC</i>	phenolic acid decarboxylase	Q: Secondary metabolites biosynthesis, transport and catabolism	1,88	Intracellular	
lp_3673	<i>pepC2</i>	aminopeptidase C	E: Amino acid transport and metabolism	1,52	Intracellular	
lp_3676	–	cell surface protein precursor, CscC family	–	-1,84	Secretory(released) (with CS)	Sec-(SPI)
lp_3687	–	Membrane protein insertase YidC 2 Foldase YidC 2 Membrane integrase YidC 2 Membrane protein YidC 2 Precursor	U: Intracellular trafficking, secretion, and vesicular transport	-1,67	Multi-transmembrane(Lipid modified N-termini)	Sec-(SPII)

^a Fold change refers to incubation in MRS supplemented with hydroxytyrosol 10 mM relative to growth in MRS lacking HXT. ^b FDR ≤ 0.05 . ^c LocateP DataBase (http://bamics2.cmbi.ru.nl/websoftware/locatep2/locatep2_start.php) CS: CleavageSite; Sec-(SPI): Secretory Pathway I; Sec-(SPII): Secretory Pathway II.